

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 4, 2002, 01:57:45 ; Search time 27.2445 Seconds

(without alignments)
1429.075 Million cell updates/sec

Title: US-09-805-550-2

Perfect score: 2036
Sequence: 1 MKLNKTKLGTGTFNEIRASPD.....EELTANYLDHGHEDDQOO 405

Scoring table: BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

- 1: p1r1:*
- 2: p1r2:*
- 3: p1r3:*
- 4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1187.5	58.3	382	2	T14336 RAD23 protein, iso
2	1127	55.4	392	2	T04150 RAD23 protein, iso
3	925.5	45.5	379	2	T14337 RAD23 protein, iso
4	840.5	41.3	367	2	P96827 protein F20B17.8
5	632	31.0	409	2	S44346 RAD23 protein, iso
6	623	30.6	385	2	UC7783 RAD 23B protein -
7	588	28.9	368	2	T40115 uv excision repair
8	573	28.1	363	2	S44443 RAD23 protein, iso
9	543	26.7	246	2	G86296 T24D18.27 protein
10	483.5	23.7	398	2	S50507 excision repair pr
11	436.5	21.4	372	2	T27774 hypothetical prote
12	361.5	17.8	113	2	H86296 F309.1 protein - A
13	229.5	11.3	551	2	C84549 probable ubiquitin
14	211	10.4	536	2	B84549 probable ubiquitin
15	202.5	9.9	502	2	T18562 hypothetical prote
16	193	9.5	142	2	T51479 hypothetical prote
17	168	8.3	373	2	S54583 ubiquitin-like pro
18	154.5	7.6	354	2	T38404 yeast dsk2 homolog
19	154.5	7.4	507	2	T44768 antifreeze glycopo
20	150.5	7.3	581	2	T22341 hypothetical prote
21	149.5	7.3	1040	2	T29092 TSC-22 protein hom
22	147.5	7.2	424	2	T33663 hypothetical prote
23	147	7.2	282	2	T18584 F15C11.2 - Caenorh
24	146	7.2	681	2	A83455 DNA polymerase sub
25	144.5	7.1	852	2	T46091 hypothetical prote
26	144.5	7.1	907	2	AD2951 cell division prot
27	144.5	7.1	910	2	H98331 cell division prot
28	144	7.1	638	1	XXAV dihydroliposamide
29	141.5	6.9	833	2	AF2089 hypothetical prote

30	141.5	6.9	2082	2	T37056 probable multi-dom
31	141	6.9	347	2	H75253 hypothetical prote
32	141	6.9	590	1	T35297 probable dihydroli
33	141	6.9	647	2	T39141 hypothetical prote
34	140.5	6.9	1116	2	S77213 DNA-directed DNA p
35	140	6.9	638	2	H82690 hypothetical prote
36	140	6.9	2440	2	S39162 transcriptional coac
37	140	6.9	2441	2	A12284 CREB-binding prote
38	139.5	6.9	1039	2	A12284 translation initia
39	139.5	6.9	1132	2	A35098 MHC class III hist
40	139	6.8	340	2	A35630 regulatory protein
41	138.5	6.8	762	2	H87302 chemotaxis protein
42	138	6.8	421	2	A60058 neural cell adhesi
43	137.5	6.8	547	2	H83018 dihydroliposamide a
44	137.5	6.8	865	2	A47282 calcium-binding pr
45	137.5	6.8	873	2	A47283 calphotin - fruit

ALIGNMENTS

RESULT 1

T14336

RAD23 protein, isoform I - carrot

C:Species: Daucus carota (carrot)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

C:Accession: T14336

R:Sturm, A.; Reinhard, S.

Plant J. 13, 815-821, 1998

A:Title: Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.

A:Reference number: Z17989; MUID:98345997; PMID:9681019

A:Accession: T14336

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-382 <STU>

A:Cross-references: EMBL:Y12013; NID:91914682; PIDN:CAA72741.1; PID:91914683

A:Experimental source: subspecies Queen Anne's lace, isolate W001C

C:Genetics:

A:Gene: RAD23-1

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match	58.3%	Score 1187.5;	DB 2;	Length 382;
Best Local Similarity	62.7%	Pred. No. 3.6e-64;		
Matches 255;	Conservative 46;	Mismatches 75;	Indels 31;	Gaps 11;
QY	1	1	1	1
Db	1	1	1	1
QY	61	1	1	1
Db	61	1	1	1
QY	118	1	1	1
Db	118	1	1	1
QY	176	1	1	1
Db	176	1	1	1
QY	235	1	1	1
Db	235	1	1	1
QY	295	1	1	1
Db	295	1	1	1
QY	355	1	1	1
Db	355	1	1	1

RESULT 2

T04150

RAD23 protein homolog - rice

C:Species: *Oryza sativa* (rice)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C:Accession: T04150

R:Schultz, J.F.; Quatrano, R.S.

Plant Mol. Biol. 34, 557-562, 1997

A:Title: Characterization and expression of a rice RAD23 gene.

A:Reference number: 208695; MUID:97369378; PMID:9225866

A:Accession: T04150

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-392 <STC>

A:Cross-references: EMBL:063530; NID:g1488296; PIDN:AA65841.1; PID:g1488297

A:Experimental source: cv. Nipponbare

C:Genetics:

A:Gene: RAD23

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match 55.4%; Score 1127; DB 2; Length 392;

Best Local Similarity 59.1%; Pred. No. 1.6e-60;

Matches 243; Conservative 48; Mismatches 90; Indels 30; Gaps 9;

QY 1 MKLVNKTGKTNFEIADSPADYADVKRIETGOGSTYRADQOMLIYQKLIKDETTLE 60

DB 1 MKISVTKLGSTFOIENVDSNOKVADVKRIETGOGHIYPAEQOMLIHQKVLKDDTTLD 60

QY 61 SNGVAENFLVIMLSKAKASSGASTATKAPATLAOP--AAPVAPASVARTPTQAPV 118

DB 61 ENKVLNENFLVIMLRGKSSSS--SAPATSKAPSNQAPPTQVAPPA-----SOAPV 111

QY 119 AATAP-----PSYQAPAPATVATDADYVSOASNLVFGNNLEQTIQOILDMGG 173

DB 112 APATVPVVSATPTATSPAPAVASSEADNYGATSLVAGSLNLEATIOSILEMGG 171

QY 174 THERDTVVALRAVNNPERAIDYLSGTPENVEAOPVARAPAGQOTN--QOASPAQPA 232

DB 172 IYDRDVTALHALSAFNNPERAVEYLSGVPEQMDI--PV--PPPSIOPAPPTQASQATOPA 228

QY 233 VALPVQSPASGPNANPLIPFGVSGSNPGVPCAGSGGLDLRLQOLPOFALLOV 292

DB 229 A-----PSTLSSGPNASPLDLPPOALPNASTD-----AGGLGLMLDLRNNAQPFRTLLSV 278

QY 293 QANPOLQELKQNPQILRLIOENQAEFLRLVNESPEGPGGNIIGOLAAVPTQL 352

DB 279 QANPOLQELKQNPQILRLIOENQAEFLRLVNESPEGPGGNIIGOLAAVPTQL 352

QY 353 TTPPEREALIQLEKGFNRRLVLEFPACNKDELTANYLLDGHGHEPDDQ 403

DB 339 AVTPEDEALIRLEPMGFDRALVLDVFACNKDEQLAANYLLDHMEFADE 389

RESULT 3

T14337

RAD23 protein, isoform II - carrot

C:Species: *Daucus carota* (carrot)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

C:Accession: T14337

R:Sturm, A.; Leinhardt, S.

Plant J. 13, 815-821, 1998

A:Title: Two isoforms of plant RAD23 complement a UV-sensitive rad23 mutant in yeast.

A:Reference number: 217989; MUID:98345997; PMID:9681019

A:Accession: T14337

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-379 <STU>

A:Cross-references: EMBL:Y12014; NID:g1914684; PIDN:CAA72742.1; PID:g1914685

A:Experimental source: subspecies Queen Anne's lace, isolate W001C

C:Genetics:

A:Gene: RAD23-2

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match

45.5%; Score 925.5; DB 2; Length 379;

Best Local Similarity 50.2%; Pred. No. 1.8e-48;

Matches 203; Conservative 57; Mismatches 117; Indels 27; Gaps 8;

QY 1 MKLVNKTGKTNFEIADSPADYADVKRIETGOGSTYRADQOMLIYQKLIKDETTLE 60

DB 1 MKLVNKTGKTNFEIADSPADYADVKRIETGOGHIYPAEQOMLIHQKVLKDDTTLD 60

QY 61 SNGVAENFLVIMLSKAKASSGASTATKAPATLAOP--AAPVAPASVARTPTQAPV 119

DB 61 ESKISEDGLVYVLMGKSKMSSTGTPTAOSSSAPATTPAPAPAPAPAPAPASAVIPT 120

QY 120 TAEAPPSVQOQAPAPATVAAADADYVSOASNLVFGNNLEQTIQOILDMGGHEPDD 179

DB 121 TVEAP--LSPAPAP-----SDTYGEAASNVVAGNSNLEQTIQHIDMGGMMDTN 169

QY 180 VVALAAANNPRAIDYLSGTPENVEA--PYAPAPAGQOTNQOASAPAPAPAPVQ 238

DB 170 VSRALRAAYNNPRAVDYLSGTPENVEA--PYAPAPAGQOTNQOASAPAPAPVQ 223

QY 239 PSPASGPNANPLIPFGVSGSNPGVPCAGSGALDLRLQOLPOFALLOVQANPOI 298

DB 224 -GAAPAPNSPLNMPPOETLSC-----VTGAGLSTLEFLRNPPQFOTLRSHVQANPOI 276

QY 299 LQPMLELQKQNPQILRLIOENQAEFLRLVNESPEGPGGNIIGOLAAVPTQLVTPPE 358

DB 277 LQPMLELQKQNPQILRLIOENQAEFLRLVNESPEGPGGNIIGOLAAVPTQLVTPPE 335

QY 359 REAIQRLKGFNRRLVLEFPACNKDELTANYLLDGHGHEPDD 402

DB 336 QEAIRLEAMGFDRGLVLEAFACDRNEELAVYLLNAGDEPD 379

RESULT 4

protein F20B17.8 [imported] - Arabidopsis thaliana

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002

C:Accession: F96827

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Corn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, J.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Marzla, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96827

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-367 <STO>

A:Cross-references: GB:AE05173; NID:g7715605; PIDN:AA68123.1; GSPDB:GN00141

C:Genetics:

A:Gene: F20B17.8

A:Map position: 1

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match

41.3%; Score 840.5; DB 2; Length 367;

Best Local Similarity 47.4%; Pred. No. 2.2e-43;

Matches 192; Conservative 53; Mismatches 119; Indels 41; Gaps 8;

QY 1 MKLVNKTGKTNFEIADSPADYADVKRIETGOGSTYRADQOMLIYQKLIKDETTLE 60

DB 1 MKLVNKTGKTNFEIADSPADYADVKRIETGOGHIYPAEQOMLIHQKVLKDDTTLD 60

QY 61 SNGVAENFLVIMLSKAKASSGASTATKAPATLAOP--AAPVAPASVARTPTQAPV 120

DB 61 ENKVLNENFLVIMLRGKSSSS--SAPATSKAPSNQAPPTQVAPPA-----SOAPV 116

[illegible]

A:Molecule type: DNA
A:Residues: 1-363 <LAMP>
A:Cross-references: EMBL:AD000092; PIDN:AAB51177.1
A:Experimental source: cell line 5HL2-B; fibroblast C:Genetics:
A:Gene: RAD23A
A:Map position: 19p13.2
A:Introns: 24/3; 78/3; 139/2; 158/1; 200/3; 227/1; 271/3; 326/3
C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology F:3-82/Domains: ubiquitin homology <UBH>

Query Match 28.1%; Score 573; DB 2; Length 363;
Best Local Similarity 33.3%; Pred. No. 2,4e-27;
Matches 139; Conservative 79; Mismatches 124; Indels 76; Gaps 13;

OY 3 LNWRLKGTNFIEISPPASVADVARIETTGCGSTYRADOQMLYGGRIKLDETTLESN 62
| : |||| : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 5 ITLKTLDOOTFKIRIMEPEDEVVLKEIKELAEGRDAFPVAGOKLYACKRIISDDPIRDY 64

OY 63 GVAESFIVIMLSKAKSSGSGATATTAKAPATTLAQPA---PVPASAVARPTQAFAVA 119
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 65 RIDENEFVVAVWTKRKA---GGGISAPPDASTTAAPESTSPAPATGMSHP--PAA 118

OY 120 TAETAPE---PSVQQAAPAATVAATDADVDYSQASNLVFNNLEQTIOQLIDMGSGT 174
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 119 REDKSPEESAAPTSPESV-SGSVPSGSGSREEDPAALTVLGSEYETMLEIMSNG--- 174

OY 175 MERDVVALTAAYNVNPERAIDLXSGTPENVENQAPVARAPACQ-QINQOASAPSAVAY 233
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 175 YERENVVALLRVSYNNPRHAEVLLTGIPGE-----PEHGVSQSQVSEDPATRA- 226

OY 234 ALPVPSPASAGPNANPLNTLPFGVPSGSGNPGVYPAGASGLDALRLQPLFOALLQLVQ 293
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 227 -----AGENPLEFLRLRQPQPOFNMRQVIQ 249

OY 294 ANPOLQPMLOELGKNQPOLRLIOENQAEPLRLYNESPESGPGCNT-----IGQLAAA 347
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 250 QNPALLPALLOOLGOENPOLLOQISRHOEFTQMNEPP--GELADIIVEGEGEVAIGEE 307

OY 348 VPQT--LVTFPEERAIORLEGMGFRRELVEVPACKKDDELTYNYLLDHGCHRDDQ 403
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 308 APQMYIOTVTOEKAIERLKALGFPESLVIOAFACEKNENTLANFL--SQNDDE 363

RESULT 9
G86296
C:Species: Arabidopsis thaliana
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text-change 27-Nov-2001
C:Accession: G86296
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federpihl, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzai, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.M.; Luros, J.S.; Matl, R.; Marziani,
Rizzo, M.; Rooney, T.E.; Rowley, D.; Sakano, H.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <STO>
A:Cross-references: GB:AE005172; NID:96597822; PIDN:AAF18513.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 26.7%; Score 543; DB 2; Length 246;
Best Local Similarity 41.8%; Pred. No. 9.6e-26;
Matches 117; Conservative 41; Mismatches 74; Indels 48; Gaps 4;

Db 228 ---LCPEONIDN-----VDEGNDNLNLANPQALAEITALLQONPEMLA 269

Qy 301 PMLDELGNQONPQILRLIOENQAEFLRLVNESPGGPGNIIQLQALAAVPOQLT----- 353

Db 270 AVLQGLAAVNPRLVQTIQNNQCAFMDLLNGAGGA-----GAAAGNAPERPTPRRHVH 323

Qy 354 VTPEREALQRLGNGFN--RELVLVEFFACKDEELANTYLLDH 396

Db 324 LSPERAAAIERIKAIYVNAPEAVVEAYFACDKNEAIAINFETSN 368

RESULT 12

H86296

F309.1 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001

C:Accession: H86296

R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, Chlu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cready, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

C.A.: Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Martzalli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: H86296

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-113 <STO>

A:Cross-references: GB:AE005172; NID:94966345; PIDN:AMD34676.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 17.88; Score 361.5; DB 2; Length 113;

Best Local Similarity 61.18; Pred. No. 2.9e-15;

Matches 69; Conservative 22; Mismatches 21; Indels 1; Gaps 1;

Qy 291 LVQANPQILQMLDELGNQONPQILRLIOENQAEFLRLVNESPGGPG-NILGQLAAV 349

Db 1 MVNSNPQILQMLDELGNQONPQILRLIOENQAEFLRLVNESPGGPGSDVDITFDQPDQEMP 60

Qy 350 QTLVTPEREALQRLGNGFNRELVLVEFFACKNDEELANTYLLDHGHEPD 402

Db 61 HSNVTPEREALQRLGNGFNRELVLVEFFACKNDEELANTYLLDHGHEPD 113

RESULT 13

C84549

Probable ubiquitin-like protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84549

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84549

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-551 <STO>

A:Cross-references: GB:AE002093; NID:94584343; PIDN:AMD25138.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g17200

A:Map position: 2

Query Match 11.3%; Score 229.5; DB 2; Length 551;

Best Local Similarity 23.7%; Pred. No. 1.6e-06;

Matches 132; Conservative 61; Mismatches 170; Indels 193; Gaps 26;

Qy 3 INVKTILKGTNFEIEASPDASVADVRRIETTGOSTYRADQMLTYOGKILKDETTLESN 62

Db 20 VNIROSNGTKFSVKTSLDSTVESFKEIVAQS---SDVPANQRLIYKGRILKDDQFTLSY 76

Qy 63 GVAENSLYIMLSKAKASSGASTATTAKAPATLQAPAPAPASVARTPQAPVATAE 122

Db 77 GIQADH--TIHWVRSAPSS-----APPAPASQTTAPASVTRGVGSD 117

Qy 123 TA-----PPSVQOAPAPATVATDDADY 147

Db 118 NSSNLGASPGESLPFGAGFNPGLGGNMSGIFGAGLPDLYVQOQLQONPMITDM--IN 176

Qy 148 SCAPASNLVFGNNLE-----QTIOQLDMG---GGTWERDVTYVRLRAVNPPE--- 192

Db 177 TPAIQNLN--NNPEFRSMINNNPQMRRELYDNPGLHYLNDPSILRQTLBAARNPELMR 234

Qy 193 ---RAIDLYISGP-----ENVEAQVAPAPAGQQTNOQASPAQAV--- 233

Db 235 EMKRTTDRAMSNIESMPREGFNMLRMVENVQEPPLNATTMSGNAGNNTGSPFALLGNQ 294

Qy 234 ALPVPSPAS-----AG---PNANPLNLPPOGVPSG-----GSNPGV-- 267

Db 295 GYTTGSGDASNNSTPNNAGTGTTPANPLP--NPKATGQQTAPERTVNGDANSFGLG 353

Qy 268 VPGAGS-----GA-----LDALRQLPQALQVQANPQI-----L 299

Db 354 LGGISLGLGIGLGLMGADSPGLGATPPDASQSLQLQNPALISQMGSVSPNPNQMLMSL 413

Qy 300 QPMLDELGNQONPQILRLIOENQAEFLRLVNESPE----- 333

Db 414 NPQLRSMDSNPQLREMMQ--NPDLRQFS--SPEMMQOMTLQOSLSONRNTASODACOT 470

Qy 334 ---GGPG-----NILGQLAA---AVPQTLVTPEREAL--IQRLEMGF--NRELVLVE 378

Db 471 GAATGNNNGGLDILMMFQSLGAGLSTGNSVNPPEERATQQLQDLMGFTDRANETRA 530

Qy 379 FFACKNDEELANTYLL 394

Db 531 LLATNGNVNAVERLL 546

RESULT 14

B84549

Probable ubiquitin-like protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: B84549

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: B84549

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-536 <STO>

A:Cross-references: GB:AE002093; NID:94584342; PIDN:AMD25137.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g17190

A:Map position: 2

Query Match 10.4%; Score 211; DB 2; Length 536;

Best Local Similarity 21.5%; Pred. No. 2e-05;

Matches 125; Conservative 56; Mismatches 142; Indels 258; Gaps 23;

Qy 3 INVKTILKGTNFEIEASPDASVADVRRIETTGOSTYRADQMLTYOGKILKDETTLESN 62

Db 20 VNIROSNGTKFSVKTSLDSTVESFKEIQAQ---NSDVPANQRLIYKGRILKDDQFTLSY 76

Qy 63 GVAENSLYIMLSKAKASSGASTATTAKAPATLQAPAPAPASVARTPQAPVATAE 122

